

C 2 179 83.6 329 50 A1682287 WC51C01.x  
 C 3 168 78.5 380 36 A631916 NP78B10.s  
 C 4 160 74.8 375 35 A576209 NP56F11.s  
 C 5 160 74.8 642 48 A155774 PT2.1.7-G  
 C 6 142 66.4 322 36 A660586 NP30H03.s  
 C 7 129 60.3 294 46 A117931 CG5E07.x  
 C 8 127 59.3 760 48 A1557719 PT2.1.10-  
 C 9 125 58.4 378 39 A660587 NP47G12.s  
 C 10 76 35.5 370 63 A592246 A197206 wr42d04.x  
 C 11 53 24.8 545 103 A630331 A605931 RPEC11-3  
 C 12 20 9.3 276 59 A660586 A608286 A608286  
 C 13 19 8.9 421 41 A105651 cy96d10.x  
 C 14 18 8.4 272 42 A1147724 qb43d09.x  
 C 15 18 8.4 326 28 A6081449 zno6G06.x  
 C 16 18 8.4 522 39 A6635226 A6635226 ak6b06.s  
 C 17 18 8.4 546 47 A1467857 A1667857 cy83902.x  
 C 18 17 7.9 268 74 A6346924 A6346924 M110686  
 C 19 17 7.9 266 74 A6208037 A6208037 qh82a09.x  
 C 20 17 7.9 292 43 A1243504 A1243504 y664h05.s  
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 C 23 17 7.9 391 100 A6312074 A6312074 RPEC11-93  
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 C 25 17 7.9 408 105 A6620046 A6620046 HS-5186-A  
 C 26 17 7.9 427 88 A6877464 A6877464 HS-2146-A  
 C 27 17 7.9 441 91 A6145997 A6145997 HS-2226-A  
 C 28 17 7.9 443 25 N70966 N70966 za3c02.s1  
 C 29 17 7.9 462 87 A6815740 A6815740 HS-5283-B  
 C 30 17 7.9 468 104 A6555758 A6555758 HS-5230-B  
 C 31 17 7.9 484 24 N31364 A1197315 yx54G06.r1  
 C 32 17 7.9 485 30 A1197315 zq50F03.s  
 C 33 17 7.9 490 43 A1162663 A1162663 A6219327-  
 C 34 17 7.9 506 62 A1903753 A1903753 IL-BR037-  
 C 35 17 7.9 516 22 H11831 H11831 ym11h07.r1  
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 C 37 17 7.9 527 99 A6234569 A6234569 HS-2054-A  
 C 38 17 7.9 531 87 A60805277 A60805277 HS-3214-A  
 C 39 17 7.9 541 100 A6313844 A6313844 RPEC11-94  
 C 40 17 7.9 544 104 A6563558 A6563558 HS-3343-A  
 C 41 17 7.9 544 49 A1632528 A1632528 wbl0b03.x  
 C 42 17 7.9 546 103 A6479186 A6479186 RPEC11-11-2  
 C 43 17 7.9 554 64 A6022746 A6022746 df43a12.Y  
 C 44 17 7.9 554 64 A6022746 A6022746 df43a12.Y  
 C 45 17 7.9 566 81 B67277 B67277 T2N3TR TAM

## ALIGNMENTS

RESULT 1  
 A1792251 369 bp mRNA EST 02-JUL-1999  
 LOCUS np78b10.y5 NCI-CGAP-Pr2 Homo sapiens cDNA clone IMAGE:1133411  
 DEFINITION: np78b10.y5 NCI-CGAP-Pr2 Homo sapiens cDNA clone IMAGE:1133411  
 similar to contains Alu repetitive element; contains element MER4  
 repetitive element ; mRNA sequence.

ACCESSION A1792251 GI:5339967  
 VERSION A1792251.1  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 369)  
 NCI/NCICGAP http://www.nci.nih.gov/ncicgap.  
 National Cancer Institute / National Institute of Dental Research,  
 Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished (1997)  
 On Jun 5, 1998 this sequence version replaced gi:3187227.  
 Other ESTs: np78b10.x5  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui,

M.D., Michael Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Kitzman, Ph.D.  
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLN at:  
 www.bio.lnl.gov/bbrp/image/image.html

This read is a RESEQUENCE of a previously sequenced human clone  
 Original clone citation: see original entry for original citation  
 Information  
 This 5' resequenced clone has no previous 5' data to verify this  
 new read against  
 Putative full length read  
 The vector to vector length is 370  
 Seq primer: -40RP from Gibco.

## FEATURES

source  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1132411"  
 /clone\_lib="NCI-CGAP-Pr2"  
 /sex="Male"  
 /dev\_stage="45 years old"  
 /lab\_host="DH10B"  
 /note="vector: PAM10; Site 1: NotI; Site 2: EcoRI; 1st  
 strand cDNA was primed with oligo(dT)17 on 50 ng of  
 DNase-treated, total cellular RNA obtained from  
 5,000-10,000 microdissected preneoplastic cells  
 histologically-determined to be prostatic intraepithelial  
 neoplasia 2 (PIN2) cells. Double-stranded cDNA was  
 ligated to EcoRI adaptors, 5 cycles of PCR applied to the  
 cDNA with an adaptor specific primer, and the resulting  
 PCR product subcloned into pAMP10 by the UDG-cloning  
 method (Life Technologies). Average insert size is 600  
 bp. NOTE: Not directionally cloned. This library was  
 constructed by David Kitzman."

## BASE COUNT

101 a 88 c 93 g 87 t

Query Match 99.1%; Score 212; DB 60; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 7e-107;  
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGGCGTCAACAGAGCGCCACTGAGGCTGAACCTTAGGCCCATGCTGCTTCA 62  
 DB 7 AAGGCGTCAACAGAGCGCCACTGAGGCTGAACCTTAGGCCCATGCTGCTTCA 66  
 QY 63 AGGTCAAGCACTGATCTGTCCTCCACCTTTGCAGAGAGAGAGGATGTGCGC 122  
 DB 67 AGGTCAAGCACTGATCTGTCCTCCACCTTTGCAGAGAGAGAGGATGTGCGC 126  
 QY 123 CCATTCTCAGATCAAGAGCGGCCCATCTTACTACCTCCAGAGAGTCTTCTCTAA 182  
 DB 127 CCATTCTCAGATCAAGAGCGGCCCATCTTACTACCTCCAGAGAGTCTTCTCTAA 186  
 QY 183 TAGAATAACATCTTGAACATCTACTGG 214  
 DB 187 TAGAATAACATCTTGAACATCTACTGG 218

RESULT 2  
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 LOCUS WC51C01.x1 NCI-CGAP-Pr2 Homo sapiens cDNA clone IMAGE:2322144 3'  
 DEFINITION: WC51C01.x1 NCI-CGAP-Pr2 Homo sapiens cDNA clone IMAGE:2322144 3'  
 similar to contains Alu repetitive element; contains element MER4  
 repetitive element ; mRNA sequence.  
 ACCESSION A1682287  
 VERSION A1682287.1 GI:4892469  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

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2 316 93.2 642 48 AI557474 AI557474 PT2.1-7-G
3 292 86.1 329 50 AI662257 AI662257 w51c01.x
4 292 86.1 369 60 AI792251 AI792251 np78B10.y
5 292 86.1 380 60 AI691916 AI691916 np78B10.y
6 266 78.5 378 39 AA876887 AA876887 ny47512.s
7 261 77.0 294 46 AI417931 AI417931 t955607.x
8 222 65.5 760 48 AI557019 AI557019 PT2.1-10-
9 171 50.4 322 63 AA618586 AA618586 np30h03.s
10 76 22.4 370 63 AI972049 AI972049 w542d04.x
11 56 16.5 545 103 AO503937 AO503937 RPCI-11-3
12 34 10.0 531 104 AO560799 AO560799 HS-2079-B
13 30 8.8 417 90 AO038229 AO038229 CIT-HSP-2
14 30 8.8 641 79 AG012358 AG012358 Homo sapi
15 30 8.8 645 79 AG012356 AG012356 Homo sapi
16 30 8.8 652 79 AG012359 AG012359 Homo sapi
17 30 8.8 725 79 AG012570 AG012570 Homo sapi
18 30 8.8 726 79 AG012595 AG012595 Homo sapi
19 30 8.8 727 79 AG012598 AG012598 Homo sapi
20 30 8.8 742 79 AG012593 AG012593 Homo sapi
21 30 8.8 752 79 AG012594 AG012594 Homo sapi
22 29 8.6 390 24 H72049 H72049 Yr99b02.s1
23 29 8.6 397 36 AA620300 AA620300 af05g04.s
24 29 8.6 398 33 AA455041 AA455041 aa04e06.s
25 29 8.6 407 24 H73336 H73336 yu05d01.s1
26 29 8.6 504 82 AO727006 AO727006 HS-5431-A
27 27 8.0 213 25 N70900 N70900 za33a05.s1
28 27 8.0 249 104 AO586994 AO586994 RPCI-11-4
29 27 8.0 272 21 T92000 T92000 ye01c12.s1
30 27 8.0 325 37 AA702361 AA702361 z187g02.s
31 27 8.0 326 21 T96961 T96961 ye50f08.s1
32 27 8.0 337 64 AW089007 AW089007 xd34b09.x
33 27 8.0 338 35 AA588288 AA588288 no25c12.s
34 27 8.0 359 37 AA714684 AA714684 nx91h08.s
35 27 8.0 380 34 AA503720 AA503720 ne50f03.s
36 27 8.0 383 47 AI500579 AI500579 tn93b04.x
37 27 8.0 387 26 W47327 W47327 zc39c12.s1
38 27 8.0 390 47 AI522295 AI522295 t176e03.x
39 27 8.0 395 21 R02172 R02172 ye87e07.s1
40 27 8.0 396 26 W45269 W45269 zc82e09.s1
41 27 8.0 404 21 R01398 R01398 ye77a12.s1
42 27 8.0 424 26 W47326 W47326 zc39c12.s1
43 27 8.0 425 38 AA807307 AA807307 oc38a01.s
44 27 8.0 427 45 AI349788 AI349788 ta96f08.x
45 27 8.0 435 87 AO757670 AO757670 HS-2274-B
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## ALIGNMENTS

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RESULT 1
LOCUS AA578209 375 bp mRNA EST 12-SEP-1997
DEFINITION n156f11.s1 NCI-CGAP_P4 Homo sapiens CDNA clone IMAGE:1044717
similar to contains Alu repetitive element; contains element MERA
repetitive element ; mRNA sequence.
ACCESSION AA578209
VERSION AA578209.1 GI:2356393
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 375)
NCI-CGAP http://www.ncbi.nlm.nih.gov/cgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1407086.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1350
Email: Robert.Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuagui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
```

JOURNAL COMMENT

On Sep 12, 1996 this sequence version replaced gi:1407086.

CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.dlo.llnl.gov/dbp/image/image.html](http://www.dlo.llnl.gov/dbp/image/image.html)

Insert Length: 395 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham.  
Location/Qualifiers  
1. 375  
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/db\_xref="taxon:9606"  
/clone="IMAGE:1044717"  
/clone\_lib="NCI-CGAP\_P4"  
/sex="male"  
/tissue="prostate" prostatic intraepithelial neoplasia - high  
grade  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: prostate; Vector: PAMP10; mRNA made from  
prostate intraepithelial neoplasia (high-grade), CDNA  
made by oligo-dr priming. Non-directionally cloned.  
Size selected on agarose gel, average insert size 600 bp.

BASE COUNT 110 a 87 c 90 g 88 t  
ORIGIN

Query Match 100.0%; Score 339; DB 35; Length 375;  
Best Local Similarity 100.0%; Pred. No. 4.8e-169;  
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GACCAACAGAGCCGACCTGAGCTGAACCTTTAGCCGCTGCTGCTGCAAGTC 60
QY 61 AGGCAAGCTGATTCGTGCTCCACCTTGCAGAGAACAGGATGTGGCCATT 120
DB 61 AGGCAAGCTGATTCGTGCTCCACCTTGCAGAGAACAGGATGTGGCCATT 120
QY 121 TCTCAGTCAAGAGCCGACCTGCTACTCTCAAGAGTCTTCTCTCAATAGA 180
DB 121 TCTCAGTCAAGAGCCGACCTGCTACTCTCAAGAGTCTTCTCTCAATAGA 180
QY 122 TCTCAGTCAAGAGCCGACCTGCTACTCTCAAGAGTCTTCTCTCAATAGA 180
DB 122 TCTCAGTCAAGAGCCGACCTGCTACTCTCAAGAGTCTTCTCTCAATAGA 180
QY 181 AAACATCTACTTGAACATCTACTGCGAGACAGAGATGAGCTGCTGCTGTAAT 240
DB 181 AAACATCTACTTGAACATCTACTGCGAGACAGAGATGAGCTGCTGCTGTAAT 240
QY 241 CTGGAATTCGGAGGCGGAGGAGGAATTCCTGAGACAGAGTCCAGACAGCC 300
DB 241 CTGGAATTCGGAGGCGGAGGAGGAATTCCTGAGACAGAGTCCAGACAGCC 300
QY 301 TGGCAATGTAGCAAGCCTGCTCTATTATACATA 339
DB 301 TGGCAATGTAGCAAGCCTGCTCTATTATACATA 339
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RESULT 2  
LOCUS AI557474 642 bp mRNA EST 09-AUG-1999  
DEFINITION PT2.1.7.G02.r tumor2 Homo sapiens CDNA 3', mRNA sequence.  
ACCESSION AI557474  
VERSION AI557474.1 GI:4489837  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 642)  
Huang, G.M., Ng, W.L., Farkas, J., He, L., Liang, H.A., Gordon, D., Yu, J.  
and Hood, L.  
Prostate cancer expression profiling by cDNA sequencing analysis

2	184	89.8	642	48	AT557474	PT2.1-7-G
3	160	78.0	329	50	AT682287	wc51c01.x
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6	134	65.4	378	39	AA878897	np47912.s
7	131	63.9	322	36	AA649586	np30h03.s
8	129	62.9	294	46	AT411921	tg55e07.x
9	127	62.0	760	48	AT557019	PT2.1-10-
10	76	37.1	370	63	AT927206	wr42d04.x
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12	19	9.3	421	41	AT056551	oy98d10.x
13	18	8.8	272	42	AT147724	qb33d09.x
14	18	8.8	326	28	AA081449	zn06906.f
15	18	8.8	522	39	AA835226	ak55b06.s
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18	17	8.3	268	74	AM208037	M11068E
19	17	8.3	292	43	AT1243504	qb82d09.x
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22	17	8.3	386	25	D80092	HUM027D06B
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24	17	8.3	402	87	AO767933	HS_3089_A
25	17	8.3	408	105	AO620046	HS_5186_A
26	17	8.3	427	88	AO877464	HS_2146_A
27	17	8.3	441	91	AO145997	HS_2226_A
28	17	8.3	443	25	N70966	za34c02.s1
29	17	8.3	462	87	AO815740	HS_5283_B
30	17	8.3	468	104	AO555758	HS_5230_B
31	17	8.3	484	24	N31364	ys54g06.f1
32	17	8.3	485	30	AA197315	tg50f03.s
33	17	8.3	490	43	AI162663	AO21P32U
34	17	8.3	506	62	AI903753	IL-BT037-
35	17	8.3	516	22	H11831	ym11n07.f1
36	17	8.3	526	100	AO283408	RPC11-90
37	17	8.3	527	99	AO234569	HS_2054_A
38	17	8.3	541	100	AO313844	RPC11-94
39	17	8.3	541	104	AO563558	HS_5343_A
40	17	8.3	544	49	AT632528	wb10b03.x
41	17	8.3	546	103	AO479186	RPC1-11-2
42	17	8.3	554	64	AO222446	df43a12.y
43	17	8.3	566	81	B67277	T22N3TR TAM
44	17	8.3	575	104	AO507017	RPC1-11-2
45	17	8.3	579	103	AO488916	RPC1-11-2

ALIGNMENTS

RESULT 1  
1578209 375 bp mRNA EST 12-SEP-1997  
XCUS n156f11.s1 NCI-CGAP\_Pt4 Homo sapiens CDNA clone IMAGE:1044717  
DEFINITION similar to contains Alu repetitive element; contains element MERA  
repetitive element; mRNA sequence.  
VERSION AA578209.1 GI:2356393  
KEYWORDS human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 375)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
On Sep 12, 1996 this sequence version replaced gi:1407086.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuagui,

CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLN at:  
[www-bio.llnl.gov/bdpr/image/image.html](http://www-bio.llnl.gov/bdpr/image/image.html)  
Insert Length: 395 Std Error: 0.00  
Seq primer: -40ml3 fwd. RT from Amersham.  
Location/Qualifiers  
1. 375  
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/clone\_1id="NCI-CGAP\_Pt4"  
/sex="male"  
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grade"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: prostate; Vector: pAMP10; mRNA made from  
prostate intraepithelial neoplasia (high-grade), CDNA  
made by oligo-dT priming. Non-directionally cloned.  
Size-selected on agarose gel, average insert size 600 bp.

BASE COUNT 110 a 87 c 90 g 88 t  
ORIGIN  
Query Match 99.5%; Score 204; DB 35; Length 375;  
Best Local Similarity 100.0%; Pred. No. 3,4e-101;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2 CAAACAGAGCGGCGGAGGAGGCTGAACCTTTAGCGGAGCTTGTTCAGAGTCAG 61  
4 CAAACAGAGCGGCGGAGGAGGCTGAACCTTTAGCGGAGCTTGTTCAGAGTCAG 63  
62 CAGATGATTTGTGTCCTCCACCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 121  
64 CAGATGATTTGTGTCCTCCACCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 123  
122 CAGATGATTTGTGTCCTCCACCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 181  
124 CAGATGATTTGTGTCCTCCACCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 183  
182 CATCTACTTGAACATCTACTG 205  
184 CATCTACTTGAACATCTACTG 207

RESULT 2  
AT557474 642 bp mRNA EST 09-AUG-1999  
LOCUS PT2.1-G02.r tumor2 Homo sapiens CDNA 3', mRNA sequence.  
DEFINITION AT557474  
VERSION AT557474.1 GI:4489837  
KEYWORDS human.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 642)  
Huang, G.-M., Ng, W.-L., Farakas, J., He, L., Liang, H.-A., Gordon, D., Yu, J.,  
and Hood, L.  
Prostate cancer expression profiling by CDNA sequencing analysis  
Genomics 59 (2), 178-186 (1999)  
9933982  
On Jun 5, 1998 this sequence version replaced gi:3187163.  
Contact: Guyang Matthew Huang  
Jeroy Hood  
University of Washington  
Department of Molecular Biotechnology, Box 357730, University of  
Washington Seattle, WA 98195

C 2	311	89.9	329	50	..A1682287
C 3	300	86.7	380	36	..A61916
C 4	292	84.4	375	35	..A578709
C 5	292	84.4	642	48	..A1557474
C 6	261	75.4	294	46	..A444991
C 7	257	74.3	378	39	..A467697
C 8	222	64.2	760	48	..A1557019
C 9	182	52.6	322	36	..A619886
C 10	76	22.0	370	63	..A1922487
C 11	53	15.3	545	103	..A509931
C 12	34	9.8	531	104	..A636799
C 13	30	8.7	417	90	..A618227
C 14	30	8.7	641	79	..A612358
C 15	30	8.7	645	79	..A612355
C 16	30	8.7	652	79	..A612359
C 17	30	8.7	725	79	..A612370
C 18	30	8.7	726	79	..A612358
C 19	30	8.7	727	79	..A612358
C 20	30	8.7	742	79	..A612358
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C 23	29	8.4	397	36	..A620300
C 24	29	8.4	398	33	..A455041
C 25	29	8.4	407	24	..H73336
C 26	29	8.4	504	82	..A0727006
C 27	27	7.8	213	25	..N70900
C 28	27	7.8	249	104	..A0586994
C 29	27	7.8	272	21	..T92000
C 30	27	7.8	325	37	..A702361
C 31	27	7.8	326	21	..T96961
C 32	27	7.8	327	64	..A089007
C 33	27	7.8	328	35	..A588288
C 34	27	7.8	359	34	..A503720
C 35	27	7.8	383	47	..A1500579
C 36	27	7.8	387	26	..W47327
C 37	27	7.8	390	47	..A1522295
C 38	27	7.8	395	21	..R02172
C 39	27	7.8	396	26	..W45269
C 40	27	7.8	404	21	..R01398
C 41	27	7.8	424	26	..W47326
C 42	27	7.8	425	38	..AAB07307
C 43	27	7.8	427	45	..A1349788
C 44	27	7.8	435	87	..A0757670
C 45	27	7.8			

ALIGNMENTS

RESULT 1  
LOCUS A1792251  
DEFINITION np78b10.95 NCI-CGAP P12 Homo sapiens CDNA clone IMAGE:1132411  
similar to contains Alu repetitive element; contains element MER4  
repetitive element; mRNA sequence.  
ACCESSION A1792251  
VERSION A1792251.1  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 369)  
NCI/NIH-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Dental Research,  
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
On Jun 5, 1998 this sequence version replaced gi:1187227.  
OTHER ESTs: np78b10.x5  
CONTACT: Robert Strausberg, Ph.D.  
TEL: (301) 496-1550

FEATURES

source  
1..369  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1132411"  
/clone\_1db="NCI-CGAP\_P12"  
/sex="Male"  
/dev\_stage="45 years old"  
/lab\_host="DH10B"  
/note="Vector: pAMP10; Site-1: NotI; Site-2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Kitzman."

BASE COUNT

101 a 88 c 93 g 87 t

Query Match  
Best Local Similarity 100.0%; Pred. No. 2.5e-172; Indels 0; Gaps 0;  
Matches 344; Conservative

QY	3	AAGCGTGCAGAAAGAGCGCCACTGGAGGCTGAACCTTTGGCGGATGCTGCTGA	62
DB	7	AAGCGGTGCAGAAAGAGCGCCACTGGAGGCTGAACCTTTAGCCGATGCTGCTGA	66
QY	63	AGGTCAGCAAGCTGATTTGTCCTCCACCTTGGAGAGAGACAGCATGTTGCCG	122
DB	67	AGGTCAGCAAGCTGATTTGTCCTCCACCTTGGAGAGAGACAGCATGTTGCCG	126
QY	123	CCATTTTCAGATCAAGAGCCGCGCATCTACTACCTCCAGAGTCTTTCTCTAA	182
DB	127	CCATTTTCAGATCAAGAGCCGCGCATCTACTACCTCCAGAGTCTTTCTCTAA	186
QY	183	TAAAGAAACATCTACTTTGAACATCTAGGCGAGACCGAGAGTGTGCTGAGCCTG	242
DB	187	TAAAGAAACATCTACTTTGAACATCTAGGCGAGACCGAGAGTGTGCTGAGCCTG	246
QY	243	TAAATTCGAATTTGGAGGCGCGAGAGCGAGAGATCTCTTGGACAGAGATTCACAC	302
DB	247	TAAATTCGAATTTGGAGGCGCGAGAGCGAGAGATCTCTTGGACAGAGATTCACAC	306
QY	303	CAGCTGGGCAATGTGAGCAAGAGCGTGTCTATTATACATA 346	
DB	307	CAGCTGGGCAATGTGAGCAAGAGCGTGTCTATTATACATA 350	

RESULT 2  
LOCUS A1682287  
DEFINITION 329 bp mRNA  
EST  
26-MAY-1999



EX-107  
EX-108  
EX-109  
EX-110  
EX-111  
EX-112  
EX-113  
EX-114  
EX-115  
EX-116  
EX-117  
EX-118  
EX-119  
EX-120  
EX-121  
EX-122  
EX-123  
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EX-190  
EX-191  
EX-192  
EX-193  
EX-194  
EX-195  
EX-196  
EX-197  
EX-198  
EX-199  
EX-200

TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson Rk Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@atson.wustl.edu Insert Size: 742 High quality sequence stops: 258 Source: IMAGE Consortium, LUNL This clone is available royalty-free through LUNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 742 Std Error: 0.00 Seq primer: T3 High quality sequence stop: 258. Location/Qualifiers 1..387
FEATURES	
source	

all	Percent Similarity:	71.111	Percent Identity:	40.000
	Ratio:	2.406	Gaps:	1
	Quality:	77.00	Length:	455
	all	Percent scores:		

Align seg 1/1 to: T83743 from: 1 to: 387

[illegible]

seq\_name: gb\_est16:AA570478

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 495)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
Tumor Gene Index  
Unpublished (1997)  
On May 8, 1995 this sequence version replaced gi:801198.  
Chen, Y. H. H. & Chuvpilo, S. D.

JOURNAL  
COMMENT

Unpublished (1997)  
On May 8, 1995 this sequence version replaced g1:801198.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Stratagene, Inc., David B. Krizman,  
Ph.D.  
CDNA Library Array: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bdrp/image/image.html](http://www-bio.llnl.gov/bdrp/image/image.html)

```
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 440.
location/Qualifiers
1. .495
```

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1018250"
/clone_11b="NCI CGAP_Schl"
/tissue_type="Schwannoma tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; site_1: EcoRI; site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. Two
pooled bulk Schwannoma tumors. 5' adaptor sequence: 5'
GAATTCGCACGAG 3' 3' adaptor sequence: 5'
CTCGAGTGTCTTTTCTTTTCTTTT 3'. Average insert size: 1.2 kb."
BASE COUNT      134 a      129 c      114 g      118 t
ORIGIN

```

```
alignment_scores:
  Quality: 76.50      Length: 50
  Ratio: 2.250      Gaps: 2
Percent Similarity: 68.000      Percent Identity: 40.000
```

Align seg 1/1 to reverse of: AA570478 from: 1 to: 4955

10 glyprolAlHlsLeuThrHrThrsLysSerLapLeuSerAsnLys 26  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 227 GGATCCCGCTAGAGTCAGGATTCGAGATCACCCTGGCTACATGTCGAG 178  
 26 sThSerThrLeuLys...HisLeuGluGluThrArgSerasp 41  
 : ||| ||||| ||| ||| : : : : :  
 177 CCCCTTTTACAAAAATACAAAAATTGACCGGGGAT.....GTG 133  
 41 LysSerAlaCysAsnSerGlyIleSerGlyArgGlyArgLysIlePro 57  
 : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 136 CAGGCGCCCTGTATCCCAACTACTAGGAGGCCGAGGACAGAAATTCCT 87

seq\_name: gb\_gss14:AQ553229







1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE  
Tel: 33169472800  
Fax: 33160778698

email: [genexpress@genethon.fr](mailto:genexpress@genethon.fr)  
Single read, 22 T removed at sequence 5' end  
Genexpress\_library\_id: C; Genexpress\_sequence\_id: a1c-16f01  
Seq primer: (-21)M13-universal.

FEATURES	Location/Qualifiers
source	1. .331

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C-16f05"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex:Female; dev_stage=3 months old; Isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was Oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector; Clone library from B.Souares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"

```

Quality:	57.00	Length:	22
Ratio:	3.353	Gaps:	0
Percent Similarity:	77.273	Percent Identity:	50.000

alignment\_block:  
MS=00-06E-677-13 000000

Align seg 1/1 to: Z39296 from: 1 to: 331

```

5  HispHeSerApGInGlyProAlaHisLeuThrThrSerLysSerAlaPh 2
38  CATTTTACAAAGGACCATTTACATTACACAAAGATATAGCTGTA 8
21  eLeuSerAnLysLys 26
08  AATCTCAAAATAGAAA 103

```

seq\_name: gb\_est22:AI023420

seq\_documentation\_block:

LOCUS	340 bp	EST	28-AUG-1998
AI023420	mRNA		
DEFINITION	ow71g05.x1 Soares fetal_liver_spleen INFLS S1 Homo sapiens CT		

CLONE IMAGE:1652312 3', mRNA sequence.  
 AT023420  
 ACCESSION

ACCESSION	AI023420	
VERSION	AI023420.1	GI:3239826
KEYWORDS	ECT	

## KEYWORDS

## SOURCE

**ORGANIC**

Eutheria; Primates; ~~Catarrhini~~; Hominoidea: Homo

REFERENCE 1 (bases 1 to 340)

**AUTHORS** NCI-CGAP <http://www>

National Cancer Institute

Tumor Gene Index

Unpublished (1997)

11/11/11

人

LT

6

**COMMENT**

On Jan 9, 1998 this sequence version replaced gi:337906.  
Contact: Robert Stransberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Stransberg@nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAG Consortium (info@easyl.inl.gov) for further information.  
Insert Length: 911 Std Error: 0.00  
Seq. primer: 40m13 fwd. ET from Amersham  
High quality sequence stop: 332

FEATURES  
SOURCE

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1 IMAGE:1652312"
/clone_1db="Soares_fetal_liver_spleen_1NPLS-S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/db_host="DRI0B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pTR73d (Pharmacia)
with a modified polylinker; Site.1: Pac I; Site.2: Eco RI
This is a subtracted version of the original Soares fetal
liver spleen 1NPLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5'
AATCGAAGATTTATTTAAAGATCTTTTTTTTTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pTR73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

```

Quality:	57.00	Length:	22
Ratio:	3.353	Gaps:	0
Percent Similarity:	77.273	Percent Identity:	50.0000

alignment\_block:

Align seg 1/1 to: ~~A~~I023420 from: 1 to: 340

[illegible]

102 AATCTCAATAGAAA 117



2	316	93.2	642	48	11557474	PT2.1.7-G
3	292	86.1	329	50	A1682287	wecl-Q1.x
4	292	86.1	369	60	A1792257	np78D10.Y
5	292	86.1	380	36	AA631916	np78D10.s
6	266	78.5	378	39	AA876897	ny47912.s
7	261	77.0	294	46	AA777931	1455e07.x
8	222	65.5	760	48	AA557019	np7.1.10-
9	171	50.4	322	36	AA618586	np30h03.s
10	76	22.4	370	63	AA503931	RPCT-11-3
11	56	16.5	545	103	AA503931	RPCT-11-3
12	34	10.0	531	104	AA503931	RPCT-11-3
13	30	8.8	417	90	AA601235	HSP-2
14	30	8.8	641	79	AA601235	Homo sapi
15	30	8.8	645	79	AA601235	Homo sapi
16	30	8.8	652	79	AA601235	Homo sapi
17	30	8.8	725	79	AA601235	Homo sapi
18	30	8.8	726	79	AA601235	Homo sapi
19	30	8.8	727	79	AA601235	Homo sapi
20	30	8.8	752	79	AA601235	Homo sapi
21	30	8.8	752	79	AA601235	Homo sapi
22	29	8.6	390	24	AA620300	atf05904.s
23	29	8.6	397	36	AA620300	atf05904.s
24	29	8.6	398	33	AA620300	atf05904.s
25	29	8.6	407	24	AA620300	atf05904.s
26	29	8.6	504	82	AA620300	atf05904.s
27	27	8.0	213	25	AA620300	atf05904.s
28	27	8.0	249	104	AA620300	atf05904.s
29	27	8.0	272	21	AA620300	atf05904.s
30	27	8.0	325	37	AA620300	atf05904.s
31	27	8.0	326	21	AA620300	atf05904.s
32	27	8.0	327	64	AA620300	atf05904.s
33	27	8.0	328	35	AA620300	atf05904.s
34	27	8.0	359	37	AA620300	atf05904.s
35	27	8.0	380	34	AA620300	atf05904.s
36	27	8.0	383	47	AA620300	atf05904.s
37	27	8.0	387	26	AA620300	atf05904.s
38	27	8.0	390	47	AA620300	atf05904.s
39	27	8.0	395	21	AA620300	atf05904.s
40	27	8.0	396	26	AA620300	atf05904.s
41	27	8.0	404	21	AA620300	atf05904.s
42	27	8.0	424	26	AA620300	atf05904.s
43	27	8.0	425	38	AA620300	atf05904.s
44	27	8.0	427	45	AA620300	atf05904.s
45	27	8.0	435	87	AA620300	atf05904.s

ALIGNMENTS

RESULT 1  
AA578209 mRNA EST 12-SEP-1997  
LOCUS n155611.s1 NCI-CGAP\_Pt4 Homo sapiens CDNA clone IMAGE:1044717  
DEFINITION similar to contains Alu repetitive element; contains element MBR4  
repetitive element; mRNA sequence.

ACCESSION AA578209 GI:2356393  
VERSION AA578209.1 GI:2356393  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 375)  
NCI-CGAP http://www.nci.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
On Sep 12, 1996 this sequence version replaced gi:1407086.  
CONTACT: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuang,  
M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www-bio.linn.gov/dbp/image/image.html  
Insert Length: 395 Std Error: 0.00  
Seq primer: -40ml3 fwd. Ex from Amersham.  
Location/Qualifiers  
1. 375  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1044717"  
/clone\_lib="NCI-CGAP\_Pt4"  
/sex="male"  
/tissue\_type="prostatic intraepithelial neoplasia - high  
grade"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: prostate; Vector: pAMP10; mRNA made from  
prostate intraepithelial neoplasia (high-grade), CDNA  
made by oligo-dT priming. Non-directionally cloned.  
Size selected on agarose gel, average insert size 600 bp.

BASE COUNT 110 a 87 c 90 g 88 t  
ORIGIN

Query Match 100.0%; Score 339; DB 35; Length 375;  
Best local similarity 100.0%; Pred. No. 4.8e-169;  
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GACCAACAGAGCGCCACCTGGAGGCTGAACCTTAGCCGATCTGCTCAAGTC 60  
1 GACCAACAGAGCGCCACCTGGAGGCTGAACCTTAGCCGATCTGCTCAAGTC 60  
61 AGGCAAGCGATCTGCTGCTCCACCTTTGACAGAGAGAGATGTTGCGCCATT 120  
61 AGGCAAGCGATCTGCTGCTCCACCTTTGACAGAGAGAGATGTTGCGCCATT 120  
61 AGGCAAGCGATCTGCTGCTCCACCTTTGACAGAGAGAGATGTTGCGCCATT 120  
121 TCTCAGATCAAGAGCGCCGATCTTACTACCTCCAGAGAGAGATGTTGCGCCATT 180  
121 TCTCAGATCAAGAGCGCCGATCTTACTACCTCCAGAGAGAGATGTTGCGCCATT 180  
121 TCTCAGATCAAGAGCGCCGATCTTACTACCTCCAGAGAGAGATGTTGCGCCATT 180  
181 AAACATCTACTTGAACATCTCTGCGGACAGACAGAGAGATGTTGCGCCATT 240  
181 AAACATCTACTTGAACATCTCTGCGGACAGACAGAGAGATGTTGCGCCATT 240  
181 AAACATCTACTTGAACATCTCTGCGGACAGACAGAGAGATGTTGCGCCATT 240  
241 CTGGAATTTGGGAGCGCGAGAGAGATCTTGGAGCAGAGATTCACAGCAGCC 300  
241 CTGGAATTTGGGAGCGCGAGAGAGATCTTGGAGCAGAGATTCACAGCAGCC 300  
301 TGGGCATGTAGCAGAGAGAGATCTTGGAGCAGAGATTCACAGCAGCC 339  
301 TGGGCATGTAGCAGAGAGAGATCTTGGAGCAGAGATTCACAGCAGCC 339

RESULT 2  
AA57474 mRNA EST 09-AUG-1999  
LOCUS PT2.1.7.G02.r tumor2 Homo sapiens CDNA 3', mRNA sequence.  
DEFINITION  
ACCESSION AA57474 GI:4489837  
VERSION AA57474.1 GI:4489837  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 642)  
Huang, G.M., Ng, W.L., Faras, J., He, L., Liang, H.A., Gordon, D., Yu, J.  
and Hood, L.  
prostate cancer expression profiling by cDNA sequencing analysis

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/dbp/image/image.html](http://www.bio.llnl.gov/dbp/image/image.html)

Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 376.

Location/Qualifiers

1. .378  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="IMAGE:1274950"  
 /clone\_id="NCI\_CGAP\_Pr12"  
 /sex="male"  
 /tissue\_type="metastatic prostate bone lesion"  
 /lab\_host="DH10B"  
 /note="Vector: PAMPI0; mRNA made from metastatic prostate  
 lesion of the bone, CDNA made by oligo-dT priming.  
 Non-directionally cloned. Size-selected on agarose gel,  
 average insert size 600 bp. Library made by D. Kitzman,  
 NIH."

BASE COUNT 106 a 89 c 94 g 89 t

# alignment\_scores:

Quality: 298.00 Length: 57  
 Ratio: 5.228 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

# alignment\_block:

US-09-065-672-12 x AA876897

Align seg 1/1 to: AA876897 from: 1 to: 378

1 MetLeuCysAlaHisPheSerAspGlnGlyProAlaHisLeuThrThr 17  
 |||||||  
 120 ATGTTGTGCGCCCATTTCTCAGATCAAGAGCCGCCCATCTTACTACTC 169  
 17 rlysserAlaPheLeuSerAsnLysLysThrSerThrLeuLysHisLeuL 34  
 |||||||  
 170 CAAGAGTGTCTTCTCTCTAATAAACAATCTACTTGAACATCTAC 219  
 34 euglGluThrArgSerAspGlnSerAlaCysAsnSerGlyIleSerGly 50  
 |||||||  
 220 TGGCGGACGACGAGATGATGCTCAGCTGATCTGGAATTCGCGA 269  
 51 GtYArGtGtYArGtYsIlePro 57  
 |||||||  
 270 GGCCGAGCGCAGAGAAATTCT 290  
 seq\_name: gb\_est17:AA631916

# seq\_documentation\_block:

LOCUS AA631916.1 380 bp mRNA EST 30-OCT-1997  
 DEFINITION np78b10.s1 NCI-CGAP\_Pr2 Homo sapiens CDNA clone IMAGE:1132411  
 Similar to contains Alu repetitive element; contains element MERA  
 repetitive element ; mRNA sequence.

ACCESSION AA631916 GI:2554527

VERSION AA631916.1 GI:2554527

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:

AUTHORS Eutheria: Primates: Catarrhini: Hominiidae: Homo.

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

On Sep 12, 1996 this sequence version replaced gi:1406914.

Contact: Robert Strausberg, Ph.D.

Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui,  
 M.D., Michael Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: David B. Kitzman, Ph.D.  
 CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/dbp/image/image.html](http://www.bio.llnl.gov/dbp/image/image.html)

Insert Length: 470 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham.

Location/Qualifiers

1. .380  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="IMAGE:1132411"  
 /clone\_id="NCI\_CGAP\_Pr2"  
 /sex="Male"  
 /dev\_stage="45 years old"  
 /lab\_host="DH10B"  
 /note="Vector: PAMPI0; Site-1: NotI; Site-2: EcoRI; 1st  
 strand CDNA was primed with oligo(dT)17 on 50 ng of  
 DNase-treated, total cellular RNA obtained from  
 5,000-10,000 microdissected preneoplastic cells  
 histologically-determined to be prostatic intraepithelial  
 neoplasia 2 (PIN2) cells. Double-stranded CDNA was  
 ligated to EcoRI adaptors, 5 cycles of PCR applied to the  
 CDNA with an adaptor-specific primer, and the resulting  
 PCR product subcloned into PAMPI0 by the UPC-cloning  
 method (Life Technologies). Average insert size is 600  
 bp. NOTE: Not directionally cloned. This library was  
 constructed by David Kitzman."

BASE COUNT 87 a 92 c 90 g 111 t

# ORIGIN

# alignment\_scores:

Quality: 298.00 Length: 57  
 Ratio: 5.228 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

# alignment\_block:

US-09-065-672-12 x AA631916/rev

Align seg 1/1 to reverse of: AA631916 from: 1 to: 380

1 MetLeuCysAlaHisPheSerAspGlnGlyProAlaHisLeuThrThr 17  
 |||||||  
 264 ATGTTGTGCGCCCATTTCTCAGATCAAGAGCCGCCCATCTTACTACTC 215  
 17 rlysserAlaPheLeuSerAsnLysLysThrSerThrLeuLysHisLeuL 34  
 |||||||  
 214 CAAGAGTGTCTTCTCTAATAAACAATCTACTTGAACATCTAC 165  
 34 euglGluThrArgSerAspGlnSerAlaCysAsnSerGlyIleSerGly 50  
 |||||||  
 164 TGGCGGACGACGAGATGATGCTCAGCTGATCTGGAATTCGCGA 115  
 51 GtYArGtGtYArGtYsIlePro 57  
 |||||||  
 114 GGCCGAGCGCAGAGAAATTCT 94

seq\_name: gb\_est29:AI557474

# seq\_documentation\_block:

LOCUS AI557474 642 bp mRNA EST 09-AUG-1999  
 DEFINITION PT2.1-7.G02.r tumor2 Homo sapiens CDNA 3', mRNA sequence.

ACCESSION AI557474 GI:4489837

VERSION AI557474.1 GI:4489837

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

11:55

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-065-672-13 x A1972251

Align seg 1/1 to: A1972251 from: 1 to: 369

1 MetleucylalaphispheseraspGlnGlyProAlaHisLeuThrThrse 17  
 |||  
 116 ATGTTGCGCCCATTTCTCAGATCAAGACCGCCCATCTTACTACTC 165

17 rlysserAlapheluserasnlysthrser 28  
 |||  
 166 CAAGAGTCTTCTCTCTAATAGAAACATCT 199

seq\_name: gb\_est37:A1972706

seq\_documentation\_block:

LOCUS A1972706 370 bp mRNA EST 25-AUG-1999  
 DEFINITION w42d04.x1 NCI\_CGAP\_P128 Homo sapiens cDNA clone IMAGE:2490343 3'  
 similar to contains Alu repetitive element;contains element MER4  
 repetitive element ;, mRNA sequence.

ACCESSION A1972706 GI:5769532  
 VERSION A1972706.1  
 KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 370)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

AUTHORS

TITLE Unpublished (1997)

JOURNAL

On Dec 20, 1995 this sequence version replaced gi:1135022.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550

COMMENT

Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/dbp/image/image.html

Seq primer: -40UP from Gibco.

FEATURES

Location/Qualifiers

1..370

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2490343"

/clone\_lib="NCI\_CGAP\_P128"

/sex="male"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Organ: prostate; Vector: p17T3D-Pac (Pharmacia)  
 with a modified polylinker; Plasmid DNA from the  
 normalized library NCI\_CGAP\_P122 was prepared, and ss  
 circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clonoids  
 985608-986759, 1101192-1101959, and 1217928-1220615).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

86 a 78 c 76 g 130 t

ORIGIN

alignment\_scores:  
Quality: 146.00

Length: 28

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-065-672-13 x A1972706/rev

Align seg 1/1 to reverse of: A1972706 from: 1 to: 370

1 MetleucylalaphispheseraspGlnGlyProAlaHisLeuThrThrse 17  
 |||  
 286 ATGTTGCGCCCATTTCTCAGATCAAGACCGCCCATCTTACTACTC 237

17 rlysserAlapheluserasnlysthrser 28  
 |||  
 236 CAAGAGTCTTCTCTCTAATAGAAACATCT 203

seq\_name: gb\_est16:AA578209

seq\_documentation\_block:

LOCUS AA578209 375 bp mRNA EST 12-SEP-1997  
 DEFINITION n156f11.s1 NCI\_CGAP\_P14 Homo sapiens cDNA clone IMAGE:1044717  
 similar to contains Alu repetitive element;contains element MER4  
 repetitive element ;, mRNA sequence.

ACCESSION AA578209 GI:2356393  
 VERSION AA578209.1  
 KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 375)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

AUTHORS

TITLE Unpublished (1997)

JOURNAL

On Sep 12, 1996 this sequence version replaced gi:1407086.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550

COMMENT

Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuagui,  
 M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Krizman, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/dbp/image/image.html

Insert Length: 395 Std Error: 0.00

FEATURES

Location/Qualifiers

1..375

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1044717"

/clone\_lib="NCI\_CGAP\_P14"

/sex="male"

/tissue\_type="prostatic intraepithelial neoplasia - high

grade"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Organ: prostate; Vector: pAMP10; mRNA made from  
 prostatic intraepithelial neoplasia (high-grade), cDNA  
 made by oligo-dT priming. Non-directionally cloned.  
 Size selected on agarose gel, average insert size 600 bp."

BASE COUNT

110 a 87 c 90 g 88 t

ORIGIN

alignment\_scores:  
Quality: 146.00  
Ratio: 5.214Length: 28  
Gaps: 0

alignment\_block:

US-09-065-672-13 x AA578209

Align seg 1/1 to: AA578209 from: 1 to: 375

1 MetleucysalapheseraspGinglyProAlaHisleuThrThrse 17  
 ||||||||||||||||||||||||||||||||||||||||||||  
 105 ATGTGTGGCCCATTTCTCAGATCAAGACCGGCCCATCTTACTACTC 154  
 ||||||||||||||||||||||||||||||||||||||||||||  
 17 rlysserAlapheluseraspnlyslslyThrser 28  
 ||||||||||||||||||||||||||||||||||||||||||||  
 155 CAAGAGTGCCTTTCTCTCTAATAGAAACATCT 188

seq\_name: gb\_est20:AA876897

seq\_documentation\_block:

LOCUS AA876897 378 bp mRNA EST 25-MAR-1998  
 DEFINITION np747912.s1 NCI\_CGAP\_P12 Homo sapiens cDNA clone IMAGE:1274950  
 similar to contains Alu repetitive element:contains element LTR3  
 repetitive element ; mRNA sequence.  
 ACCESSION AA876897  
 VERSION AA876897.1 GI:285974  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 378)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On Feb 13, 1998 this sequence version replaced gi:2761085.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,  
 Rodrigo F. Chuang, M.D., Michael R. Emmert-Buck, M.D., Ph.D.,  
 cDNA Library Preparation: David B. Kitzman, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m13 fwd. ET from AmerSham

High quality sequence stop: 376

FEATURES

source

1. 378  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="1274950"  
 /clone\_lib="NCI\_CGAP\_P12"  
 /sex="male"  
 /tissue\_type="metastatic prostate bone lesion"  
 /lab\_host="DH10B"  
 /note="Vector: pAMP10: mRNA made from metastatic prostate  
 lesion of the bone, cDNA made by oligo-dT priming.  
 Non-directionally cloned. Size-selected on agarose gel,  
 average insert size 600 bp. Library made by D. Kitzman,  
 NIH."  
 BASE COUNT 106 a 89 c 94 g 89 t  
 ORIGIN

alignment\_scores:

Quality: 146.00 Length: 28  
 Ratio: 5.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

block:  
 2-13 x AA876897

Align seg 1/1 to: AA876897 from: 1 to: 378

1 MetleucysalapheseraspGinglyProAlaHisleuThrThrse 17  
 ||||||||||||||||||||||||||||||||||||||||||||  
 120 ATGTGTGGCCCATTTCTCAGATCAAGACCGGCCCATCTTACTACTC 169  
 ||||||||||||||||||||||||||||||||||||||||||||  
 17 rlysserAlapheluseraspnlyslslyThrser 28  
 ||||||||||||||||||||||||||||||||||||||||||||  
 170 CAAGAGTGCCTTTCTCTCTAATAGAAACATCT 203

seq\_name: gb\_est17:AA631916

seq\_documentation\_block:

LOCUS AA631916 380 bp mRNA EST 30-OCT-1997  
 DEFINITION np78b10.s1 NCI\_CGAP\_P12 Homo sapiens cDNA clone IMAGE:1132411  
 similar to contains Alu repetitive element:contains element MERA  
 repetitive element ; mRNA sequence.  
 ACCESSION AA631916  
 VERSION AA631916.1 GI:254527  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 380)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1406914.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuang,  
 M.D., Michael Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Kitzman, Ph.D.  
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 470 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from AmerSham.

FEATURES

source

1. 380  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="1132411"  
 /clone\_lib="NCI\_CGAP\_P12"  
 /sex="Male"  
 /dev\_stage="45 years old"  
 /lab\_host="DH10B"  
 /note="Vector: pAMP10: Site\_1: Not1; Site\_2: EcoRI; 1st  
 strand cDNA was primed with oligo(dT)17 on 50 ng of  
 DNase-treated, total cellular RNA obtained from  
 5,000-10,000 microdissected preneoplastic cells  
 histologically determined to be prostatic intraepithelial  
 neoplasia 2 (PIN2) cells. Double-stranded cDNA was  
 ligated to EcoRI adaptors, 5 cycles of PCR applied to the  
 cDNA with an adaptor-specific primer, and the resulting  
 PCR product subcloned into pAMP10 by the UDG-cloning  
 method (Life Technologies). Average insert size is 600  
 bp. NOTE: Not directionally cloned. This library was  
 constructed by David Kitzman."  
 BASE COUNT 87 a 92 c 90 g 111 t  
 ORIGIN

alignment\_scores:

Quality: 146.00 Length: 28  
 Ratio: 5.214 Gaps: 0

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alignment_scores:
    Quality: 141.00
    Length: 27
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Quality:	141.00	Length:	27
Ratio:	5.222	Gads:	0

## alignment\_block:

US-09-065-672-14 x AA578209

Align seg 1/1 to: AA578209 from: 1 to: 375

1 ThreuleuylshleuLeuGlyGluThrArgSerAspGlySerAlaCysAs 17  
|||||  
189 ACTTGAACATCTACTGCGGACGACGAGGATGCTCAGCTGTAA 238

17 nserGlylleSerGlyLysArgGlyLys 27  
|||||  
239 TTCTGCAATTTCCGGAGCCGAGCAGGAGG 269

seq\_name: gp\_est120:AA876897

seq\_documentation\_block:

LOCUS AA876897 378 bp mRNA

DEFINITION ny77912.s1 NCI\_CGAP\_Pri12 Homo sapiens cDNA clone IMAGE:1274950  
similar to contains Alu repetitive element; contains element LTR3  
repetitive element ; mRNA sequence.

ACCESSION AA876897  
VERSION AA876897.1 GI:2985974  
KEYWORDS EST.

SOURCE

ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 378)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT On Feb 13, 1998 this sequence version replaced gi:2761085.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov  
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Dury, M.D.,  
Rodrigo F. Chuquai, M.D., Michael R. Emmert-Buck, M.D., Ph.D.,  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
www.bio.lnl.gov/bdrrp/image/image.html

Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 376.  
Location/Qualifiers

1. 378

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1274950"

/clone\_lib="NCI\_CGAP\_Pri12"

/sex="Male"

/issue\_type="metastatic prostate bone lesion"

/lab\_host="DH10B"

/note="Vector: PAMP10. mRNA made from metastatic prostate  
lesion of the bone, cDNA made by oligo-dT priming.  
Non-directionally cloned. Size-selected on agarose gel,  
average insert size 600 bp. Library made by D. Krizman,  
NH."

BASE COUNT 106 a 89 c 94 g 89 t  
ORIGIN

## alignment\_scores:

Quality: 141.00 Length: 27  
Ratio: 5.222 Gaps: 0  
Similarity: 100.000 Percent Identity: 100.000

US-09-065-672-14 x AA876897

Align seg 1/1 to: AA876897 from: 1 to: 378

1 ThreuleuylshleuLeuGlyGluThrArgSerAspGlySerAlaCysAs 17  
|||||  
204 ACTTGAACATCTACTGCGGACGACGAGGATGCTCAGCTGTAA 253

17 nserGlylleSerGlyLysArgGlyLys 27  
|||||  
254 TTCTGCAATTTCCGGAGCCGAGCAGGAGG 284

seq\_name: gp\_est17:AA631916

seq\_documentation\_block:

LOCUS AA631916 380 bp mRNA

DEFINITION np78b10.s1 NCI\_CGAP\_Pri2 Homo sapiens cDNA clone IMAGE:1132411  
similar to contains Alu repetitive element; contains element MER4  
repetitive element ; mRNA sequence.

ACCESSION AA631916  
VERSION AA631916.1 GI:2554527  
KEYWORDS EST.

SOURCE

ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 380)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT On Sep 12, 1996 this sequence version replaced gi:1406914.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov  
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquai,  
M.D., Michael Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
www.bio.lnl.gov/bdrrp/image/image.html

Insert length: 470 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham.  
Location/Qualifiers

1. 380

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1132411"

/clone\_lib="NCI\_CGAP\_Pri2"

/sex="Male"

/dev\_stage="45 years old"

/lab\_host="DH10B"

/note="Vector: PAMP10. Site 1: NotI. Site 2: EcoRI. 1st  
strand cDNA was primed with oligo(dT)17 on 50 ng of  
DNAse-treated, total cellular RNA obtained from  
5,000-10,000 microdissected preneoplastic cells  
histologically determined to be prostatic intraepithelial  
neoplasia 2 (PIN2) cells. Double-stranded cDNA was  
ligated to EcoRI adaptors, 5 cycles of PCR applied to the  
cDNA with an adaptor-specific primer, and the resulting  
PCR product subcloned into PAMP10 by the UDG-cloning  
method (Life Technologies). Average insert size is 600  
bp. NOTE: Not directionally cloned. This library was  
constructed by David Krizman."

BASE COUNT 87 a 92 c 90 g 111 t  
ORIGIN

alignment\_scores:  
Quality: 141.00 Length: 27  
Ratio: 5.222 Gaps: 0